

# Package ‘TCGAbiolinksGUI.data’

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**Title** Data for the TCGAbiolinksGUI package

**Version** 1.32.0

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**Description** Supporting data for the TCGAbiolinksGUI package.

**License** GPL-3

**LazyData** false

**Depends** R (>= 3.5.0)

**Suggests** BiocStyle, knitr, rmarkdown, readr, DT

**biocViews** AssayDomainData, TechnologyData, OrganismData

**URL** <https://github.com/BioinformaticsFMRP/TCGAbiolinksGUI.data>

**BugReports** <https://github.com/BioinformaticsFMRP/TCGAbiolinksGUI.data/issues>

**VignetteBuilder** knitr

**RoxygenNote** 7.1.2

**git\_url** <https://git.bioconductor.org/packages/TCGAbiolinksGUI.data>

**git\_branch** RELEASE\_3\_23

**git\_last\_commit** 81a8d9c

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|            |                     |
|------------|---------------------|
| GDCdisease | <i>GDC projects</i> |
|------------|---------------------|

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**Description**

Contains all GDC projects with open data

**Usage**

data("GDCdisease")

**Format**

A named list with 39 projects

**Source**

Retrieved from GDC API

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|                                     |
|-------------------------------------|
| gencode.v36.annotation.genes        |
| <i>GENCODE v36 gene information</i> |

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**Description**

GENCODE v36 gene information

**Usage**

data("gencode.v36.annotation.genes")

**Format**

A Granges object

**Source**

Downloaded from GENCODE v36 [https://www.gencodegenes.org/human/release\\_36.html](https://www.gencodegenes.org/human/release_36.html) Comprehensive gene annotation and filtered to genes

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|                    |                                      |
|--------------------|--------------------------------------|
| gene.location.hg19 | <i>Biomart hg19 gene information</i> |
|--------------------|--------------------------------------|

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**Description**

Biomart hg19 gene information

**Usage**

```
data("gene.location.hg19")
```

**Format**

A table

**Source**

Downloaded with biomaRt

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|                    |                                      |
|--------------------|--------------------------------------|
| gene.location.hg38 | <i>Biomart hg38 gene information</i> |
|--------------------|--------------------------------------|

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**Description**

Biomart hg38 gene information

**Usage**

```
data("gene.location.hg38")
```

**Format**

A table

**Source**

Downloaded with biomaRt

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|                    |                       |
|--------------------|-----------------------|
| glioma.gcimp.model | <i>gcimp RF model</i> |
|--------------------|-----------------------|

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**Description**

A RF model able to classify DNA methylation samples in to GCIMP groups

**Usage**

```
data("glioma.gcimp.model")
```

**Format**

A random forest model with 276 samples and 145 predictors classifying into 3 classes

**Source**

RF model created from DNA methylation signatures retrieved from [www.cell.com/cell/abstract/S0092-8674\(15\)01692-X](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

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|                  |                     |
|------------------|---------------------|
| glioma.idh.model | <i>IDH RF model</i> |
|------------------|---------------------|

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**Description**

A RF model able to classify DNA methylation samples in to IDH groups

**Usage**

```
data("glioma.idh.model")
```

**Format**

A random forest model with 880 samples and 1205 predictors classifying into 6 classes

**Source**

RF model created from DNA methylation signatures retrieved from [www.cell.com/cell/abstract/S0092-8674\(15\)01692-X](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

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|                     |                        |
|---------------------|------------------------|
| glioma.idhmut.model | <i>IDHmut RF model</i> |
|---------------------|------------------------|

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**Description**

A RF model able to classify DNA methylation samples in to IDHmut groups

**Usage**

```
data("glioma.idhmut.model")
```

**Format**

A random forest model with 450 samples and 1216 predictors classifying into 3 classes

**Source**

RF model created from DNA methylation signatures retrieved from [www.cell.com/cell/abstract/S0092-8674\(15\)01692-X](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

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|                    |                       |
|--------------------|-----------------------|
| glioma.idhwt.model | <i>IDHwt RF model</i> |
|--------------------|-----------------------|

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**Description**

A RF model able to classify DNA methylation samples in to IDHwt groups

**Usage**

```
data("glioma.idhwt.model")
```

**Format**

A random forest model with 430 samples and 843 predictors classifying into 3 classes

**Source**

RF model created from DNA methylation signatures retrieved from [www.cell.com/cell/abstract/S0092-8674\(15\)01692-X](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

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|                  |                          |
|------------------|--------------------------|
| linkedOmics.data | <i>linkedOmics table</i> |
|------------------|--------------------------|

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**Description**

linkedOmics table with links

**Usage**

```
data("linkedOmics.data")
```

**Format**

A table

**Source**

Parsed from <http://linkedomics.org/login.php#dataSource>

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|           |                           |
|-----------|---------------------------|
| maf.tumor | <i>GDC open MAF files</i> |
|-----------|---------------------------|

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**Description**

Contains the list of GDC project with open MAF files available

**Usage**

```
data(maf.tumor)
```

**Format**

A named list with 33 tumors

**Source**

[https://gdc-docs.nci.nih.gov/Data/Release\\_Notes/Manifests/GDC\\_open\\_MAFs\\_manifest.txt](https://gdc-docs.nci.nih.gov/Data/Release_Notes/Manifests/GDC_open_MAFs_manifest.txt)

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probes2rm

*EPIC probes removed from newer versions*


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### Description

EPIC probes removed from newer versions that should not be used in the analysis

### Usage

```
data("probes2rm")
```

### Format

A list with 977 probes

### Source

<https://support.illumina.com/downloads/infinium-methylationepic-v1-0-product-files.html>

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TCGAbiolinksGUI.data

*Auxiliary data for TCGAbiolinksGUI package.*


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### Description

**Package:** TCGAbiolinksGUI.data provide the necessary data for TCGAbiolinksGUI glioma classifier menu. It includes the following objects:

**glioma.gcimp.model** A train model for GCIMP DNA methylation signatures.

**glioma.idhwt.model** A train model for IDHwt DNA methylation signatures

**glioma.idhmut.model** A train model for IDHmut DNA methylation signatures

**glioma.idh.model** A train model for IDH DNA methylation signatures

**probes2rm** List of probes that should be removed from EPIC array due to different versions of the platform.

Source: <https://support.illumina.com/downloads/infinium-methylationepic-v1-0-product-files.html>

**maf.tumor** TCGA projects with open MAF files retrieved from the NCI's Genomic Data Commons (GDC).

Source: [https://gdc-docs.nci.nih.gov/Data/Release\\_Notes/Manifests/GDC\\_open\\_MAFs\\_manifest.txt](https://gdc-docs.nci.nih.gov/Data/Release_Notes/Manifests/GDC_open_MAFs_manifest.txt)

**GDCdisease** The NCI's Genomic Data Commons (GDC) projects list

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